



PATENT
Docket No. 511582002410

#8

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Tami M. Procopio
Tami M. Procopio

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In the application of:

Arthur B. RAITANO, *et al.*

Serial No.: 10/017,066

Filing Date: 14 December 2001

For: NOVEL G PROTEIN-COUPLED
RECEPTOR UP-REGULATED IN
PROSTATE CANCER AND USES
THEREOF

Examiner: To Be Assigned

Group Art Unit: 1642

SUBMISSION OF SUBSTITUTE DRAWINGS

Assistant Commissioner for Patents
Washington, D.C. 20231

Dear Sir:

Attached please find 27 sheet(s) of substitute drawings in connection with the above-identified application.

Respectfully submitted,

Kate H. Murashige

Dated: May 28, 2002

By: Kate H. Murashige
Registration No. 29,959

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FIG. 1A

9 18 27 36 45 54
 CAG AGA GGC TGT ATT TCA GTG CAG CCT GCC AGA CCT CTT CTG GAG GAA GAC TGG
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 63 72 81 90 99 108
 ACA AAG GGG GTC ACA CAT TCC TTC CAT ACG GTT GAG CCT CTA CCT GCC TGG TGC
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 117 126 135 144 153 162
 TGG TCA CAG TTC AGC TTC TTC ATG ATG GTG GAT CCC AAT GGC AAT GAA TCC AGT
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 M M V D P N G N E S S
 171 180 189 198 207 216
 GCT ACA TAC TTC ATC CTA ATA GGC CTC CCT GGT TTA GAA GAG GCT CAG TTC TGG
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 A T Y F I L I G L P G L E E A Q F W
 225 234 243 252 261 270
 TTG GCC TTC CCA TTG TGC TCC CTC TAC CTT ATT GCT GTG CTA GGT AAC TTG ACA
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 L A F P L C S L Y L I A V L G N L T
 279 288 297 306 315 324
 ATC ATC TAC ATT GTG CGG ACT GAG CAC AGC CTG CAT GAG CCC ATG TAT ATA TTT
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 I I Y I V R T E H S L H E P M Y I F
 333 342 351 360 369 378
 CTT TGC ATG CTT TCA GGC ATT GAC ATC CTC ATC TCC ACC TCA TCC ATG CCC AAA
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 L C M L S G I D I L I S T S S M P K
 387 396 405 414 423 432
 ATG CTG GCC ATC TTC TGG TTC AAT TCC ACT ACC ATC CAG TTT GAT GCT TGT CTG
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 M L A I F W F N S T T I Q F D A C L
 441 450 459 468 477 486
 CTA CAG ATT TTT GCC ATC CAC TCC TTA TCT GGC ATG GAA TCC ACA GTG CTG CTG
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 L Q I F A I H S L S G M E S T V L L
 495 504 513 522 531 540
 GCC ATG GCT TTT GAC CGC TAT GTG GCC ATC TGT CAC CCA CTG CGC CAT GCC ACA
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 A M A F D R Y V A I C H P L R H A T
 549 558 567 576 585 594
 GTA CTT ACG TTG CCT CGT GTC ACC AAA ATT GGT GTG GCT GCT GTG GTG CGG GGG
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 V L T L P R V T K I G V A A V V R G
 603 612 621 630 639 648
 GCT GCA CTG ATG GCA CCC CTT CCT GTC TTC ATC AAG CAG CTG CCC TTC TGC CGC
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 A A L M A P L P V F I K Q L P F C R

FIG. 1B

657	666	675	684	693	702
TCC AAT ATC CTT TCC CAT TCC TAC TGC CTA CAC CAA GAT GTC ATG AAG CTG GCC					
S N I L S H S Y C L H Q D V M K L A					
711	720	729	738	747	756
TGT GAT GAT ATC CGG GTC AAT GTC GTC TAT GGC CTT ATC GTC ATC ATC TCC GCC					
C D D I R V N V V Y G L	I V I I S A				
765	774	783	792	801	810
ATT GGC CTG GAC TCA CTT CTC ATC TCC TTC TCA TAT CTG CTT ATT CTT AAG ACT					
I G L D S L L I S F S Y L L I L K	T				
819	828	837	846	855	864
GTG TTG GGC TTG ACA CGT GAA GCC CAG GCC AAG GCA TTT GGC ACT TGC GTC TCT					
V L G L T R E A Q A K A	F G T C V S				
873	882	891	900	909	918
CAT GTG TGT GCT GTG TTC ATA TTC TAT GTA CCT TTC ATT GGA TTG TCC ATG GTG					
H V C A V F I F Y V P F I G L S M	V				
927	936	945	954	963	972
CAT CGC TTT AGC AAG CGG CGT GAC TCT CCG CTG CCC GTC ATC TTG GCC AAT ATC					
H R F S K R R D S P	L P V I L A N I				
981	990	999	1008	1017	1026
TAT CTG CTG GTT CCT CCT GTG CTC AAC CCA ATT GTC TAT GGA GTG AAG ACA AAG					
Y L L V P P V L N P I V Y G V	K T K				
1035	1044	1053	1062	1071	1080
GAG ATT CGA CAG CGC ATC CTT CGA CTT TTC CAT GTG GCC ACA CAC GCT TCA GAG					
E I R Q R I L R L F H V A T H A S E					
1089	1098	1107	1116	1125	1134
CCC TAG GTG TCA GTG ATC AAA CTT CTT TTC CAT TCA GAG TCC TCT GAT TCA GAT					
P *					
1143	1152	1161	1170	1179	1188
TTT AAT GTT AAC ATT TTG GAA GAC AGT ATT CAG AAA AAA AAT TTC CTT AAT AAA					
1197	1206	1215	1224	1233	1242
AAA TAC AAC TCA GAT CCT TCA AAT ATG AAA CTG GTT GGG GAA TCT CCA TTT TTT					
1251	1260	1269	1278	1287	1296
CAA TAT TAT TTT CTT CTT TGT TTT CTT GCT ACA TAT AAT TAT TAA TAC CCT GAC					
1305	1314	1323	1332	1341	1350
TAG GTT GTG GTT GGA GGG TTA TTA CTT TTC ATT TTA CCA TGC AGT CCA AAT CTA					

FIG. 1C

1359	1368	1377	1386	1395	1404
AAC TGC TTC	TAC TGA TGG	TTT ACA GCA	TTC TGA GAT	AAG AAT GGT	ACA TCT AGA
1413	1422	1431	1440	1449	1458
GAA CAT TTG	CCA AAG GCC	TAA GCA CGG	CAA AGG AAA	ATA AAC ACA	GAA TAT AAT
1467	1476	1485	1494	1503	1512
AAA ATG AGA	TAA TCT AGC	TTA AAA CTA	TAA CTT CCT	CTT CAG AAC	TCC CAA CCA
1521	1530	1539	1548	1557	1566
CAT TGG ATC	TCA GAA AAA	TGC TGT CTT	CAA AAT GAC	TTC TAC AGA	GAA GAA ATA
1575	1584	1593	1602	1611	1620
ATT TTT CCT	CTG GAC ACT	AGC ACT TAA	GGG GAA GAT	TGG AAG TAA	AGC CTT GAA
1629	1638	1647	1656	1665	1674
AAG AGT ACA	TTT ACC TAC	GTT AAT GAA	AGT TGA CAC	ACT GTT CTG	AGA GTT TTC
1683	1692	1701	1710	1719	1728
ACA GCA TAT	GGA CCC TGT	TTT TCC TAT	TTA ATT TTC	TTA TCA ACC	CTT TAA TTA
1737	1746	1755	1764	1773	1782
GGC AAA GAT	ATT ATT AGT	ACC CTC ATT	GTA GCC ATG	GGA AAA TTG	ATG TTC AGT
1791	1800	1809	1818	1827	1836
GGG GAT CAG	TGA ATT AAA	TGG GGT CAT	ACA AGT ATA	AAA ATT AAA	AAA AAA AAA
1845	1854	1863	1872	1881	1890
GAC TTC ATG	CCC AAT CTC	ATA TGA TGT	GGA AGA ACT	GTT AGA GAG	ACC AAC AGG
1899	1908	1917	1926	1935	1944
GTA GTG GGT	TAG AGA TTT	CCA GAG TCT	TAC ATT TTC	TAG AGG AGG	TAT TTA ATT
1953	1962	1971	1980	1989	1998
TCT TCT CAC	TCA TCC AGT	GTT GTA TTT	AGG AAT TTC	CTG GCA ACA	GAA CTC ATG
2007	2016	2025	2034	2043	2052
GCT TTA ATC	CCA CTA GCT	ATT GCT TAT	TGT CCT GGT	CCA ATT GCC	AAT TAC CTG
2061	2070	2079	2088	2097	2106
TGT CTT GGA	AGA AGT GAT	TTC TAG GTT	CAC CAT TAT	GGA AGA TTC	TTA TTC AGA
2115	2124	2133	2142	2151	2160
AAG TCT GCA	TAG GGC TTA	TAG CAA GTT	ATT TAT TTT	TAA AAG TTC	CAT AGG TGA
2169	2178	2187	2196	2205	2214
TTC TGA TAG	GCA GTG AGG	TTA GGG AGC	CAC CAG TTA	TGA TGG GAA	GTA TGG AAT
2223	2232	2241	2250	2259	2268
GGC AGG TCT	TGA AGA TAA	CAT TGG CCT	TTT GAG TGT	GAC TCG TAG	CTG GAA AGT
2277	2286	2295	2304	2313	2322
GAG GGA ATC	TTC AGG ACC	ATG CTT TAT	TTG GGG CTT	TGT GCA GTA	TGG AAC AGG
2331	2340	2349	2358	2367	2376
GAC TTT GAG	ACC AGG AAA	GCA ATC TGA	CTT AGG CAT	GGG AAT CAG	GCA TTT TTG

Genotype	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100
1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	

AAA A 3'

9 - 2

FIG. 2

1	15 16	30 31	45 46	60 61	75 76	90		
1	101P3A11	MMVDPNGNESSATYF	ILIGLPGLEEAQFWL	APPLCSLYLIAVLGN	LTIIYIVRTEHSLHE	PMYIFLCMLSGIDIL	ISTSSMPKMLAIFWF	90
2	RA1c	-MSSCN---FTHATF	MLIGIPGLEEAHFWF	GFPLLSMYAVALFGN	CIVVFIVRTERSILHA	PMYIFLCMLAAIDLA	LSTSTMPKILALFWF	86
3	HPRAJ70	-MSSCN---FTHATC	VLIIGIPGLEKAHFWV	GFPLLSMYVVMCGN	CIVVFIVRTERSILHA	PMYIFLCMLAAIDLA	LSTSTMPKILALFWF	86
	91	105 106	120 121	135 136	150 151	165 166	180	
1	101P3A11	NSTTIQFDACLLQIF	AIHSLSGMESTVLLA	MAFDRYVAICHPLRH	AFVITLPRVTKIGVA	AVVRGAALMAPLPVF	IKQLPFCRSNILSHS	180
2	RA1c	DSREITFDACLAQMF	FIHALSAIESTILLA	MAFDRYVAICHPLRH	AAVLNNTVTVOIGMV	ALVRGSLFFFPPLPLL	IKRLAFCHSNVLSHS	176
3	HPRAJ70	DSREISIEACLTQMF	FIHALSAIESTILLA	MAFDRYVAICHPLRH	AAVLNNTVTAQIGIV	AVVRGSLFFFPPLPLL	IKRLAFCHSNVLSHS	176
	181	195 196	210 211	225 226	240 241	255 256	270	
1	101P3A11	YCLHQDVMKLCDDI	RNVVYGLIIVISAI	GLDSLLISFSYLLIL	KTVLGLT-REAQAKA	FOTCVSHVCAVFIFY	VPFIGLSMVHFRFSKR	269
2	RA1c	YCVHQDVMKLAYTDT	LPNVVYGLTALLVM	GVDVMFISLSYFLII	RAVLQLPSKSERAKA	FOTCVSHIGVVLAFY	VPLIGLSVHFRFGNS	266
3	HPRAJ70	YCVHQDVMKLAYADT	LPNVVYGLTALLVM	GVDVMFISLSYFLII	RTVLQLPSKSERAKA	FOTCVSHIGVVLAFY	VPLIGLSVHFRFGNS	266
	271	285 286	300 301	315 316	330 331	345 346	360	
1	101P3A11	RDSELPVILANIYLL	VPPVLNPIIVGVKTK	EIRQRILRLFHVATH	ASEP-----	318		
2	RA1c	LDPIVHVLMGDDVYLL	LPPVINPIIYGAKTK	QIRTRVLAMFKISCD	KDIEAGGNT	320		
3	HPRAJ70	LHPIVRVVMGDIYLL	LPPVINPIIYGAKTK	QIRTRVLAMFKISCD	KDLQAVGGK	320		

FIG. 3

GATCAAACCTCTTTCCATTGAGAGTCCTCTGATTCAGATTTTAATGTTAACATTTTGGAAGACAGTATTCAGAAAAA
AATTCCTTAATAAAAAATACAACCTCAGATCCTTCAAATATGAACTGGTTGGGGAATCTCCATTTTTCAATATTATT
TCTTCTTGTTTTCTTGCTACGTATAATTATTAATATCCTGACTAGGTTGTGGTTGGAGGGTTATTACTTTTCATTTTA
CCATGCAGTCCAAATCTAAACTGCTTCTACTGATGGTTTACAGCATTCTGAGATAAGAATGGTACATCTAGAGAACATT
TGCCAAAGGCCTAAGCACAGCAAAGGAAAATAAACACAGAATATAATAAAATGAGATAATCTAGCTTAAACTATAACT
TCCTCTTTAGAACTCCCAACCACATTGATC

1000 900 800 700 600 500 400 300 200 100

FIG. 4

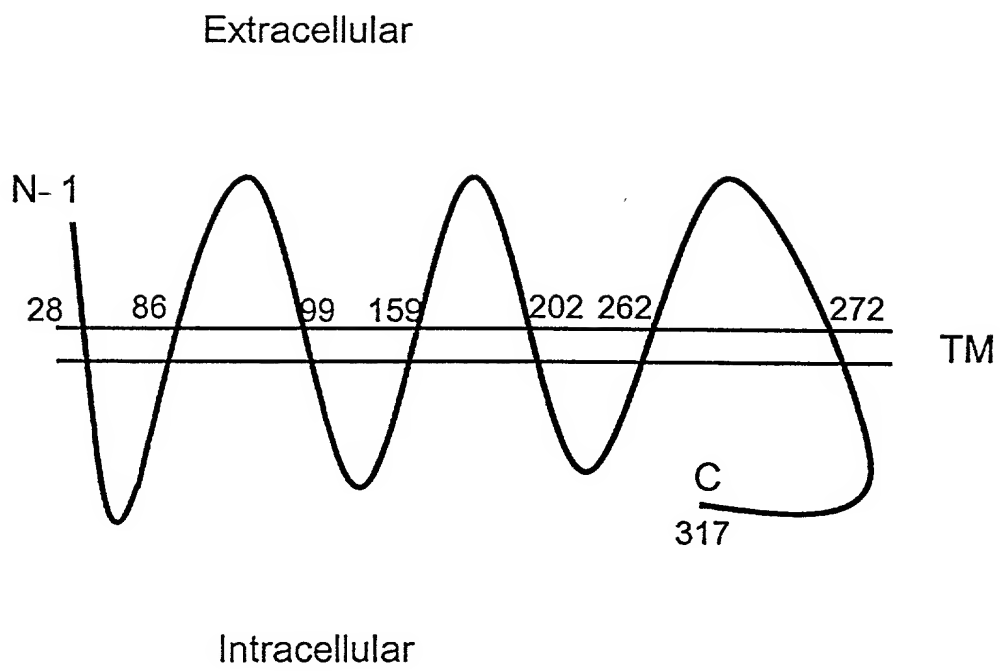


FIG. 5A

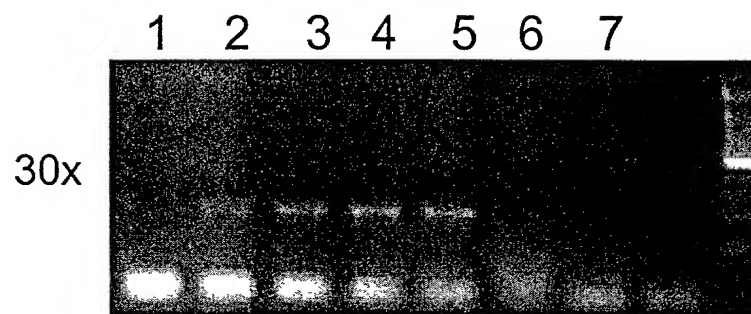


FIG. 5B

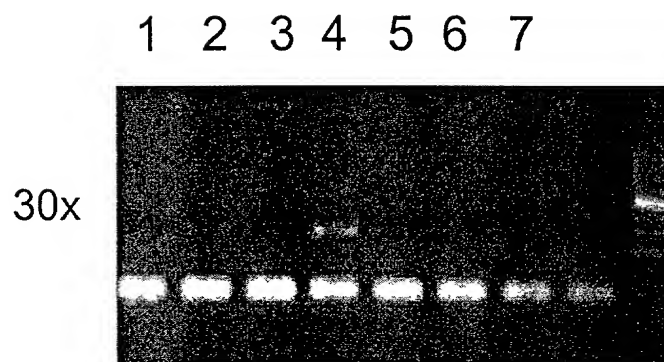


FIG. 6A

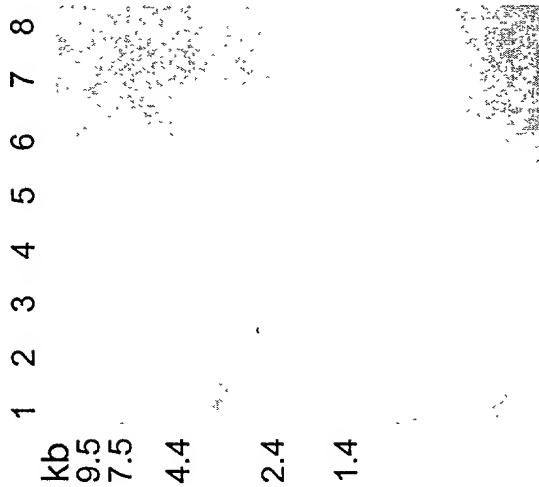


FIG. 6B

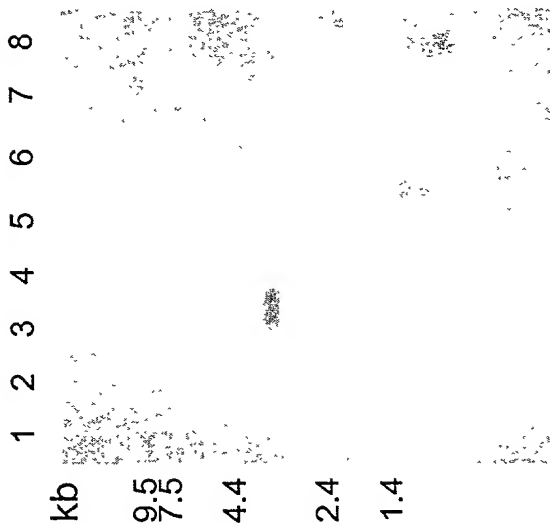


FIG. 6C

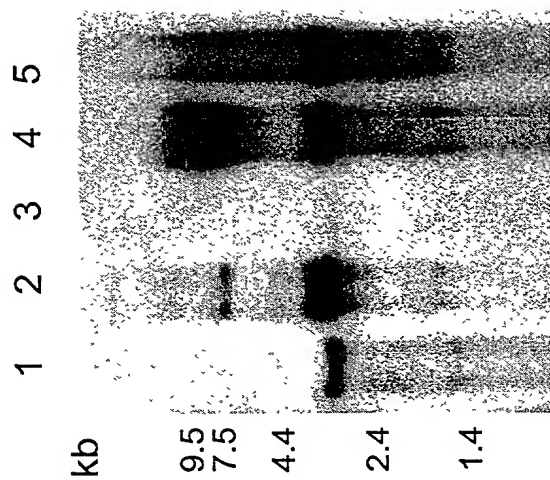


FIG. 7

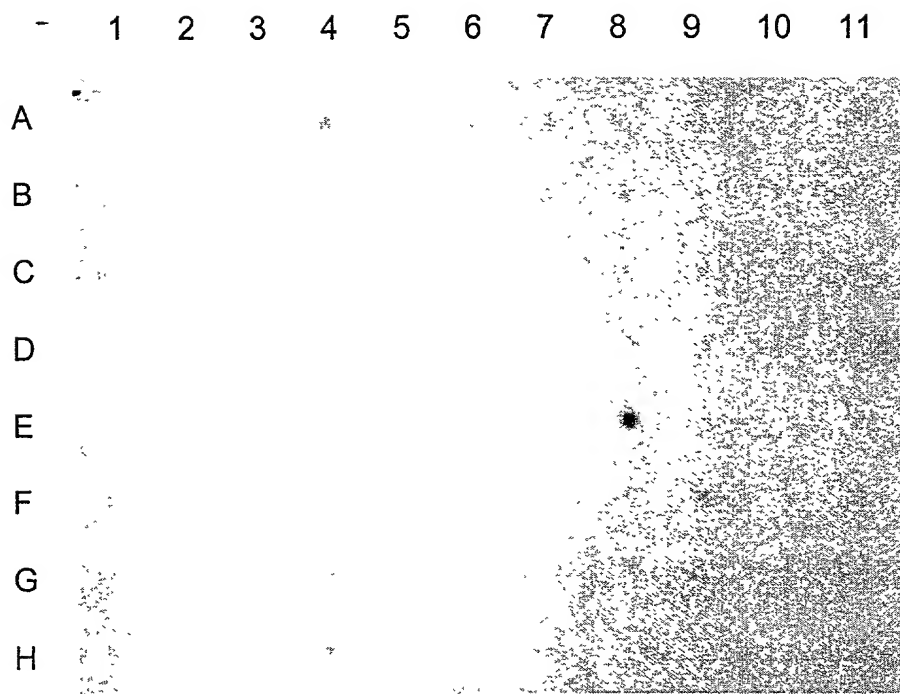


FIG. 8A

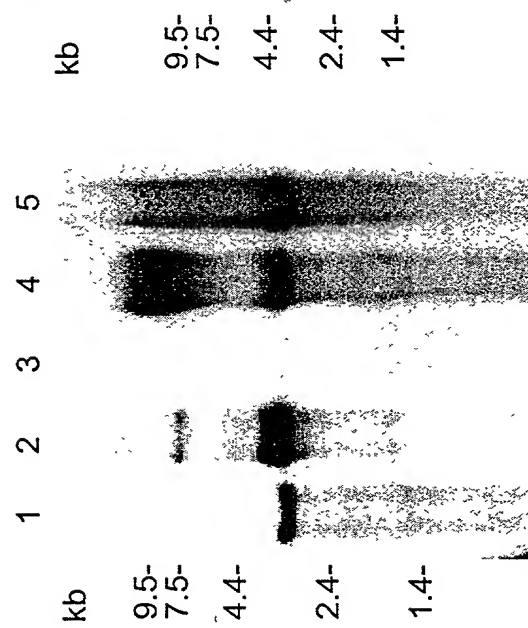


FIG. 8B

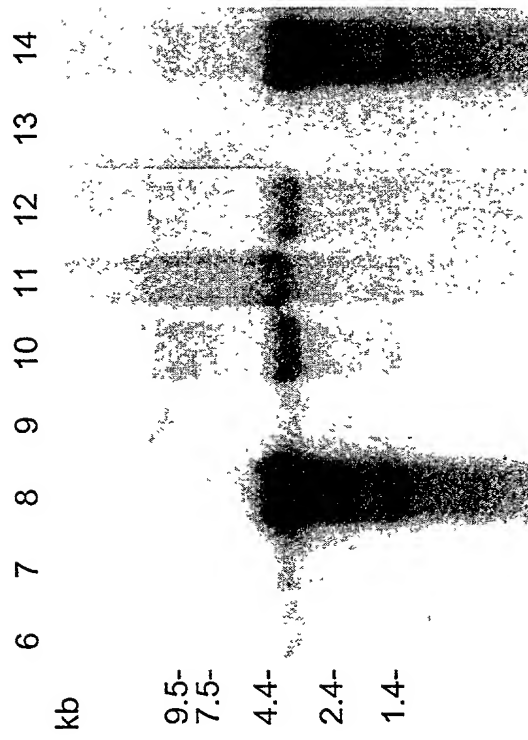


Figure 9A

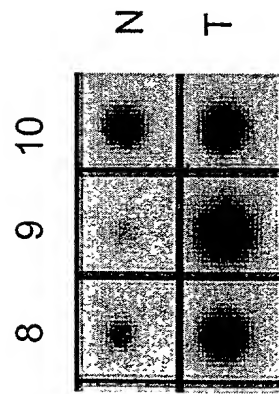
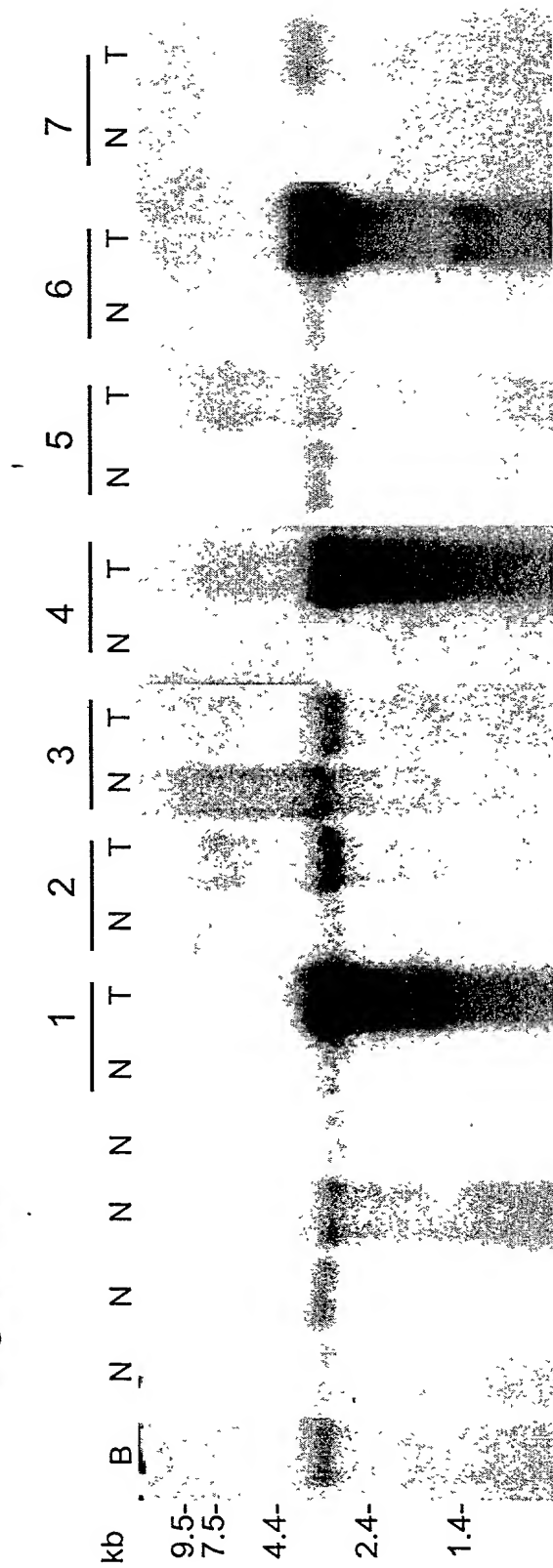


Figure 9B

Figure 10

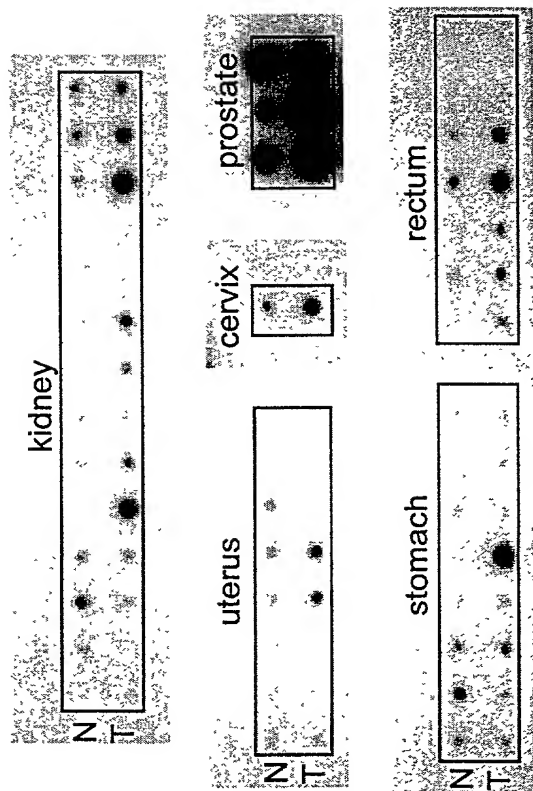


Figure 11A-11B

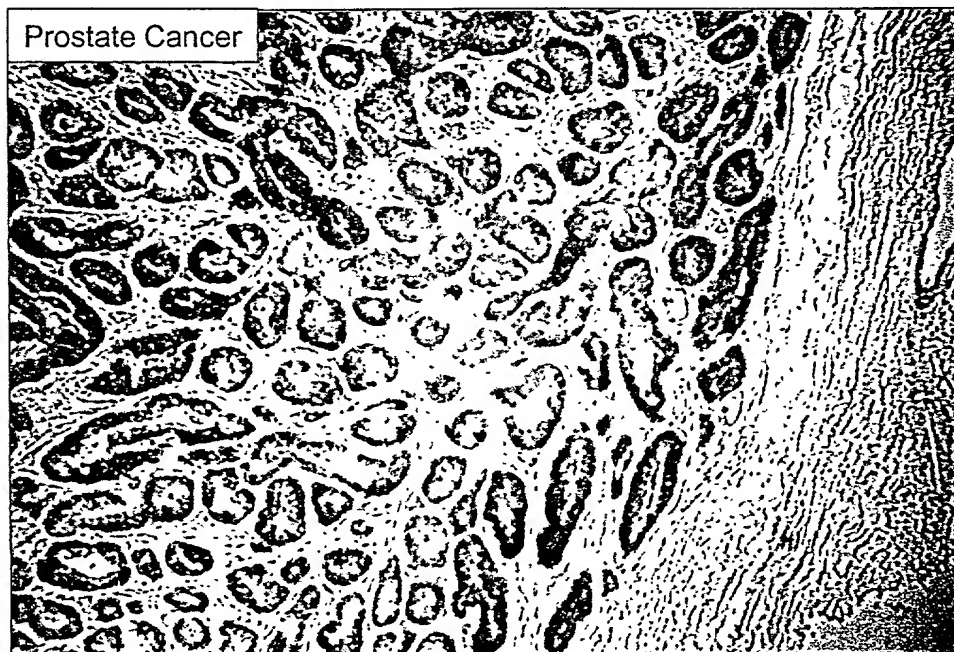
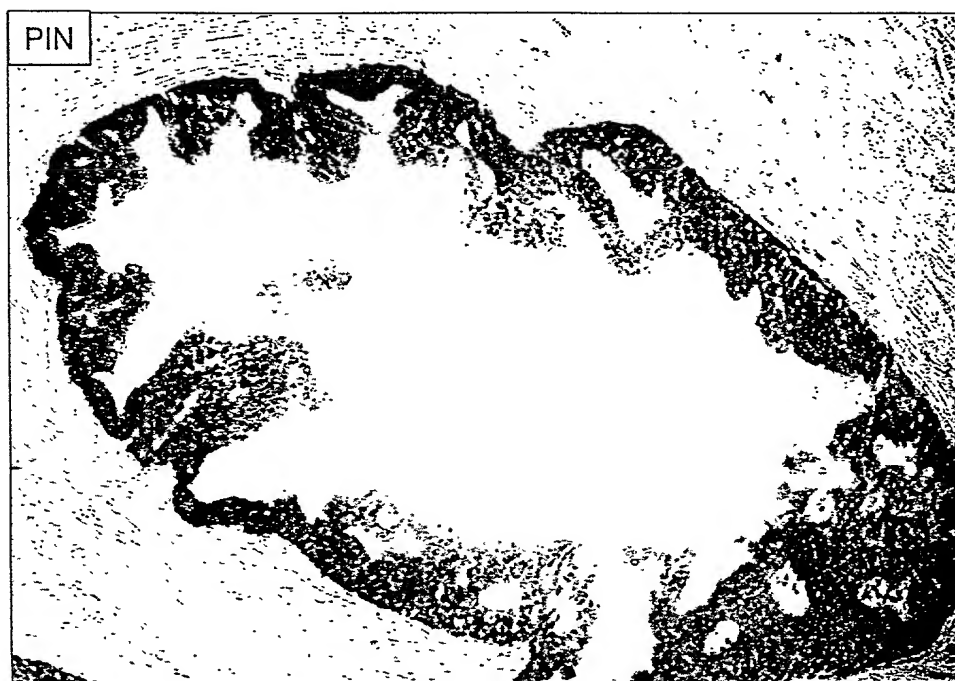


Figure 12A-12B

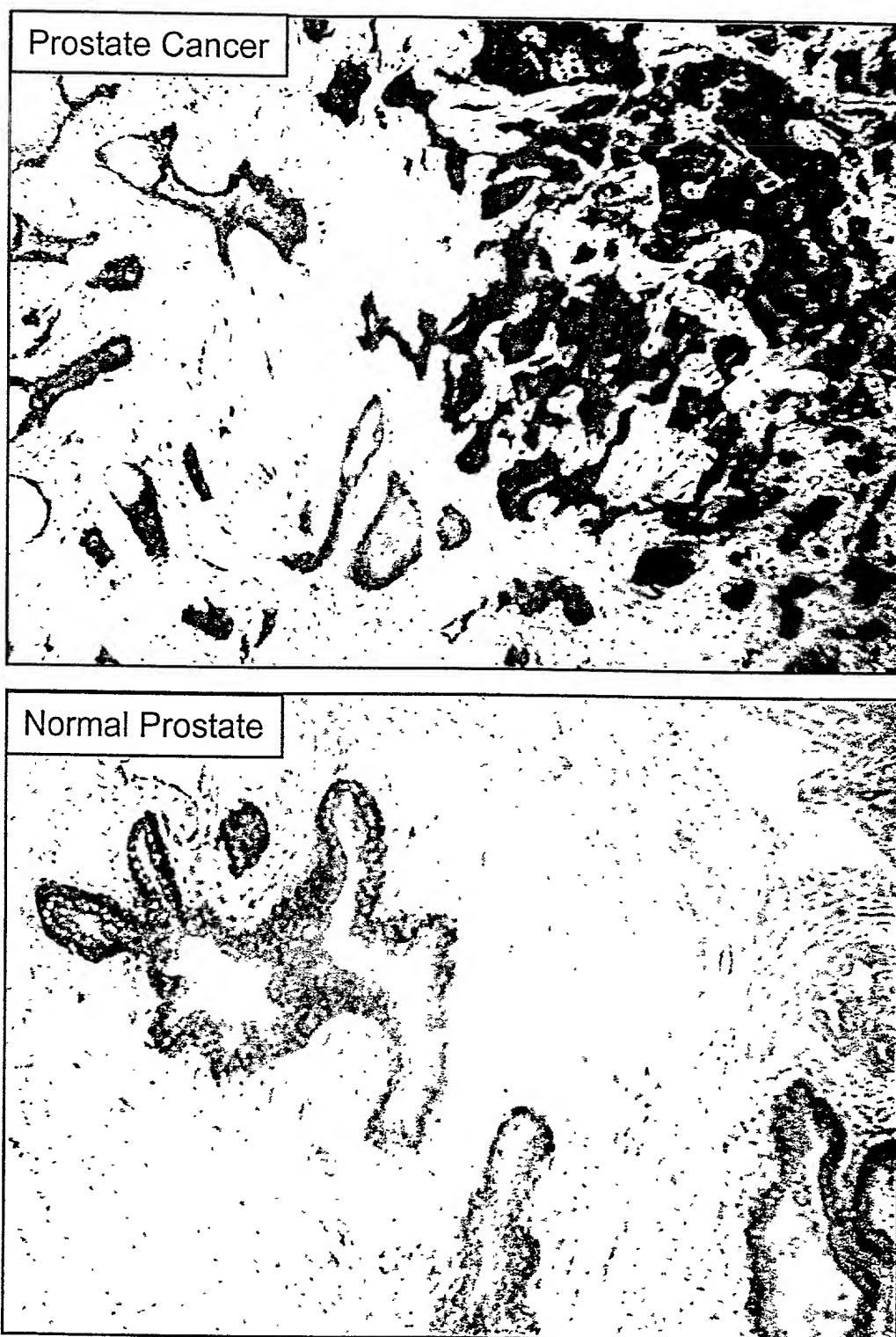


FIG. 13A

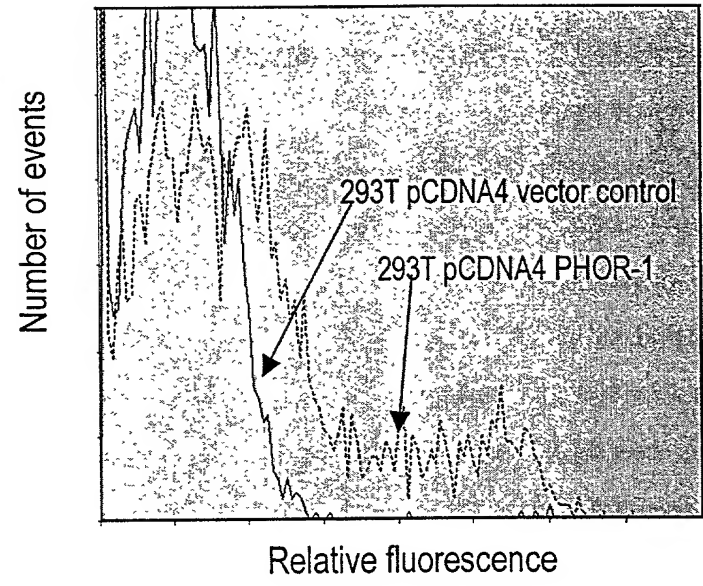


FIG. 13B

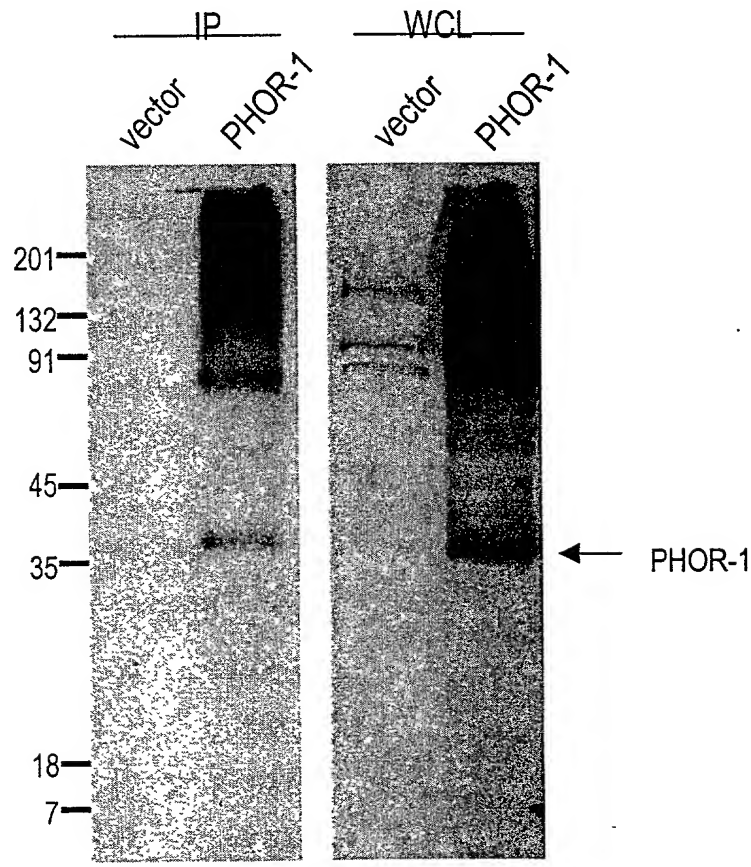


Fig. 14A

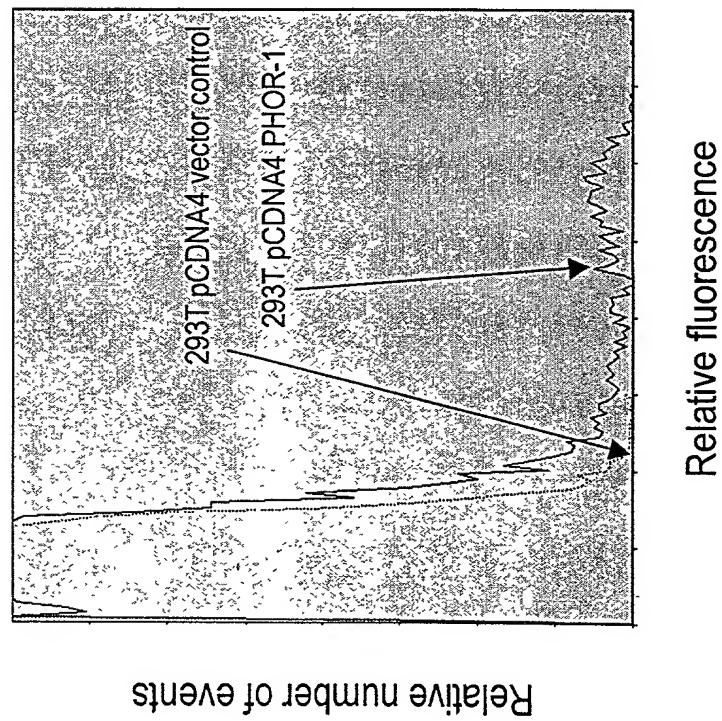


Fig. 14B

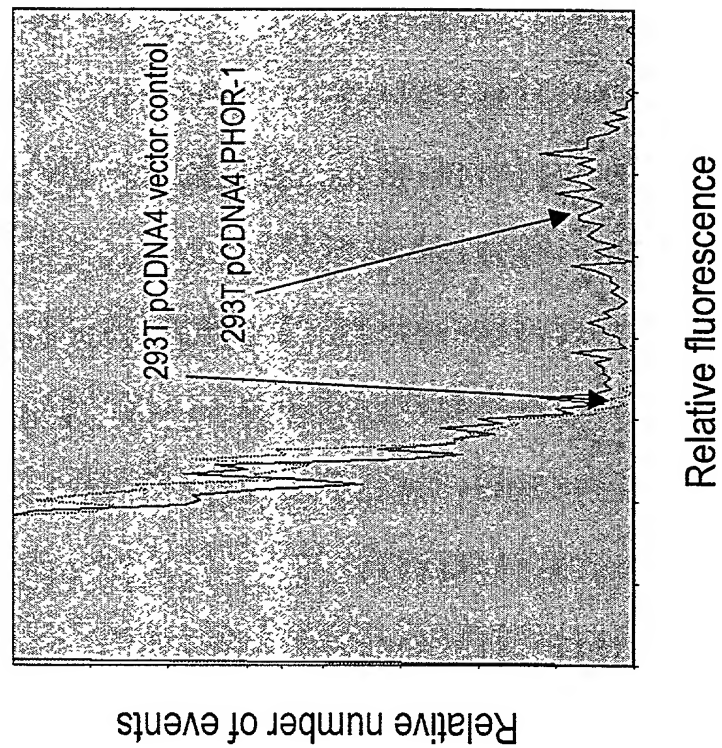


Fig. 15

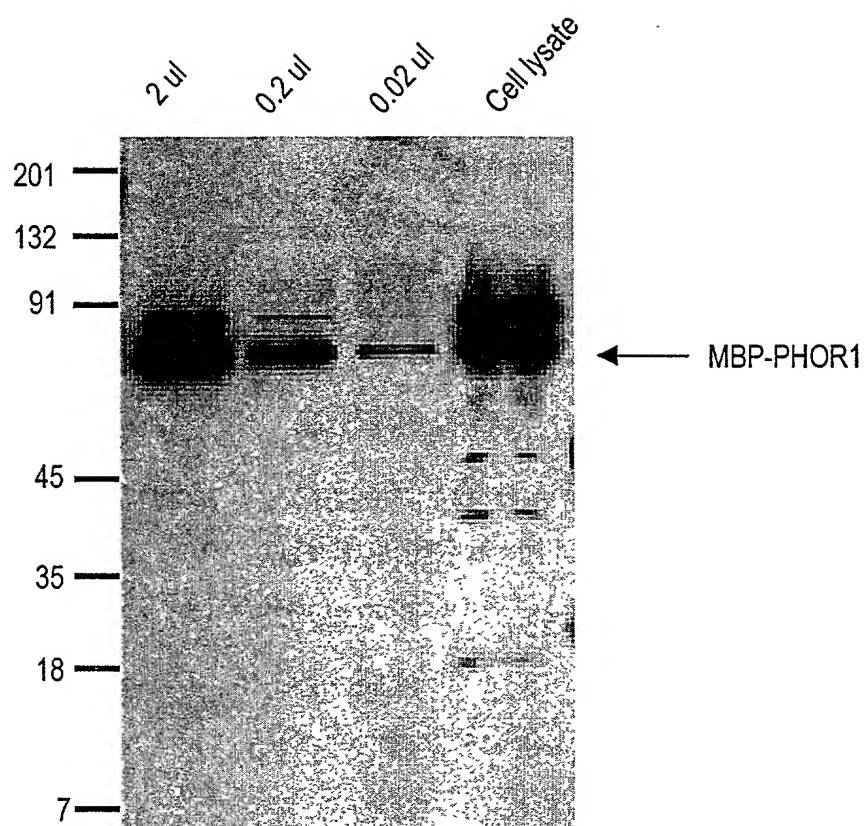


Fig. 16A

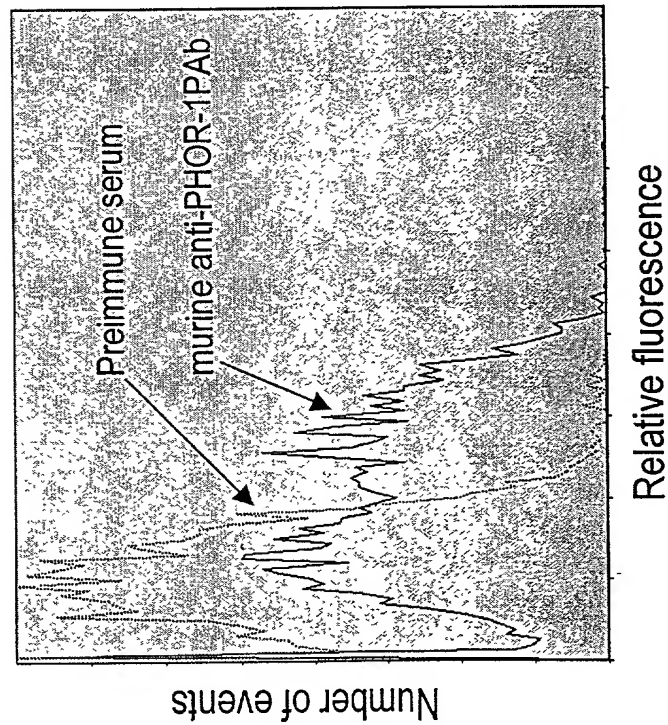
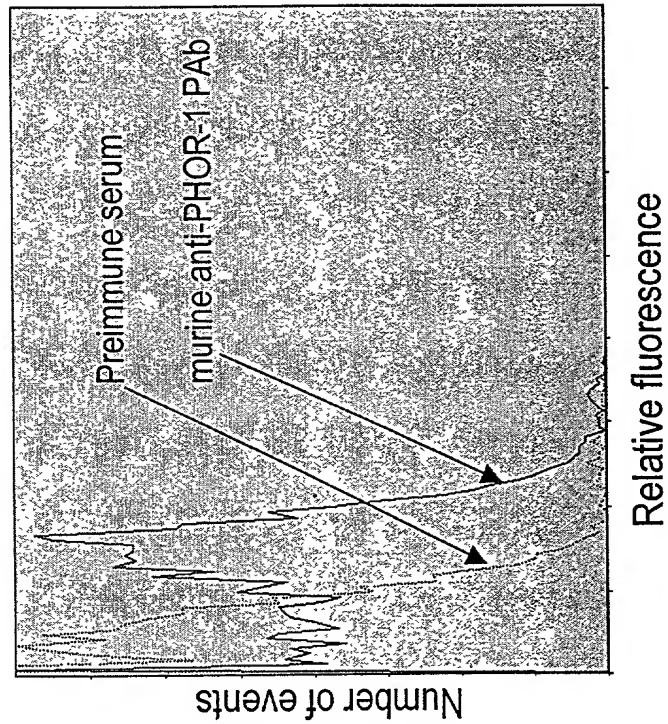


Fig. 16B



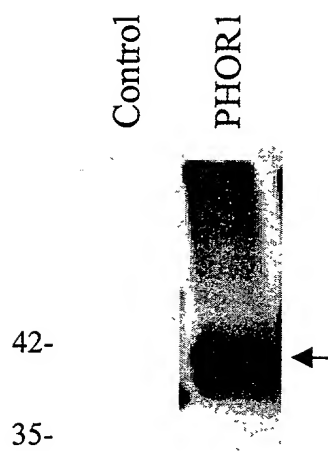


FIG. 17

Figure 18A-F

Fig. 18A. Prostate Cancer, 400X

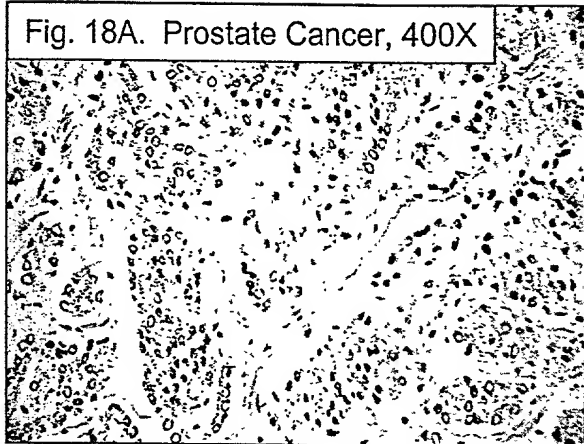


Fig. 18D. LNCaP, 400X

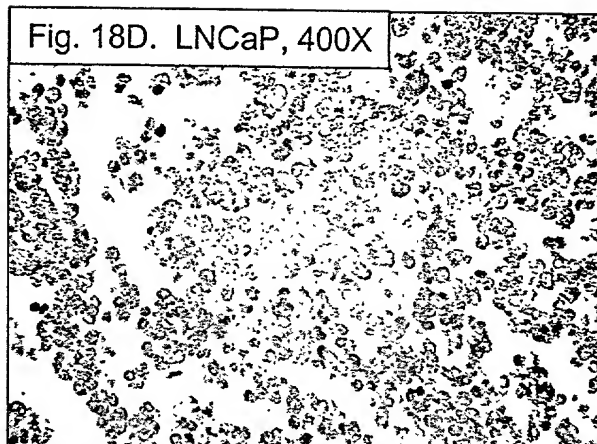


Fig. 18B. Prostate Cancer, 400X

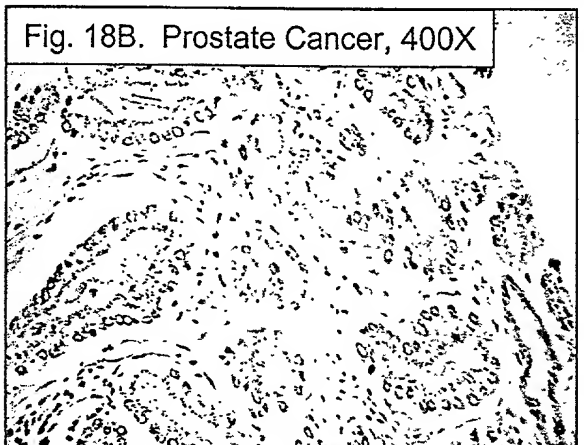


Fig. 18E. Prostate, 400X

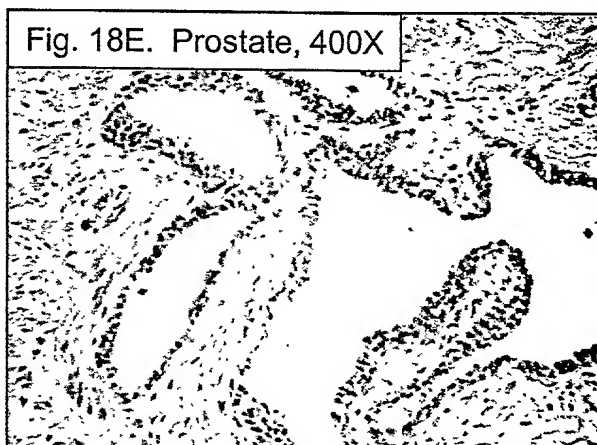


Fig. 18C. Prostate Cancer, 2000X

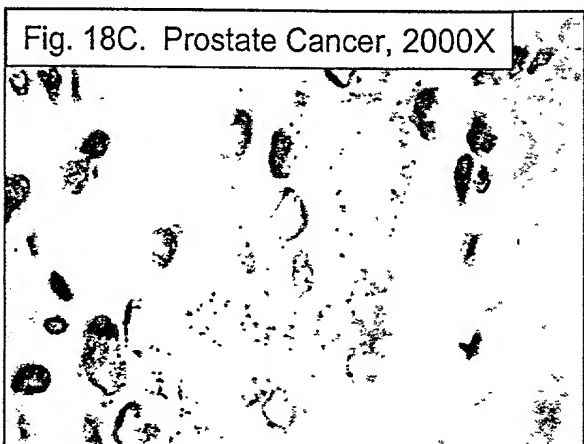


Fig. 18F. Prostate, 2000X

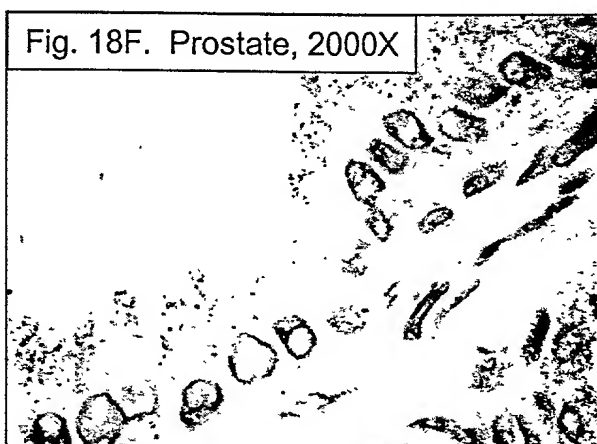


Figure 19A-F

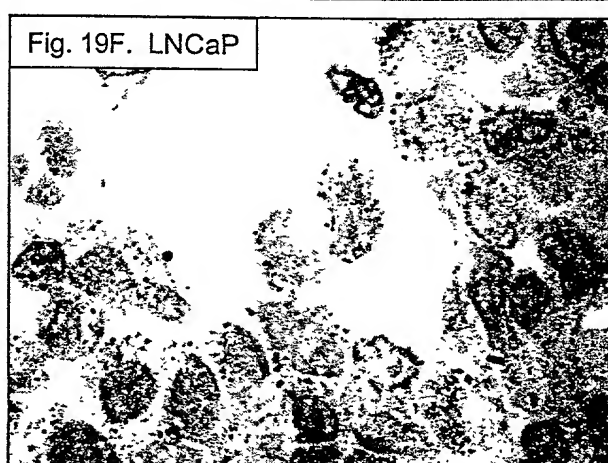
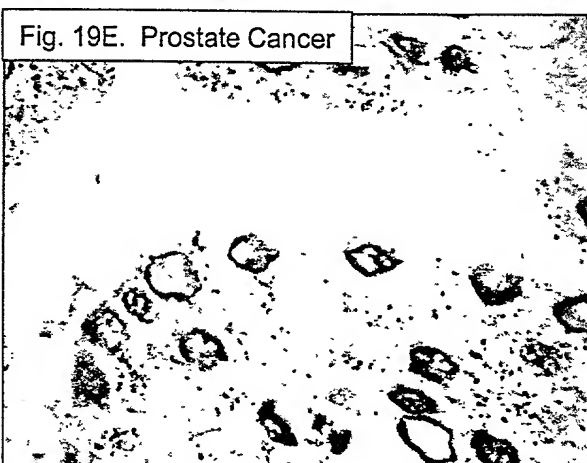
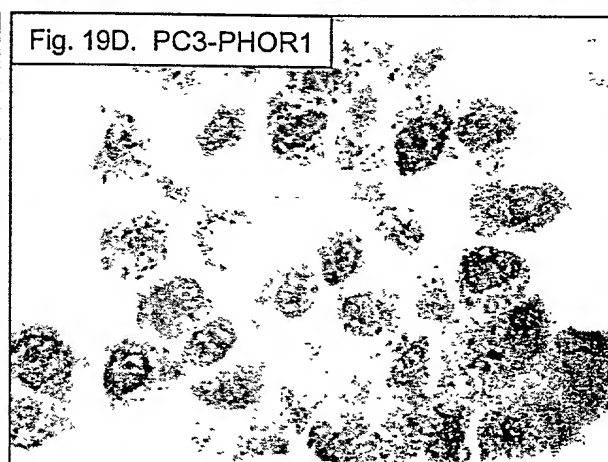
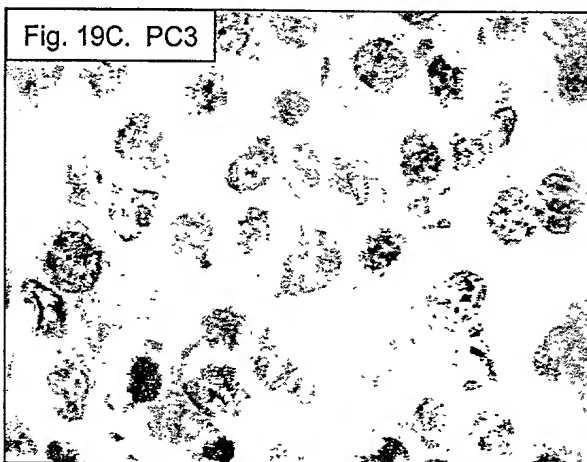
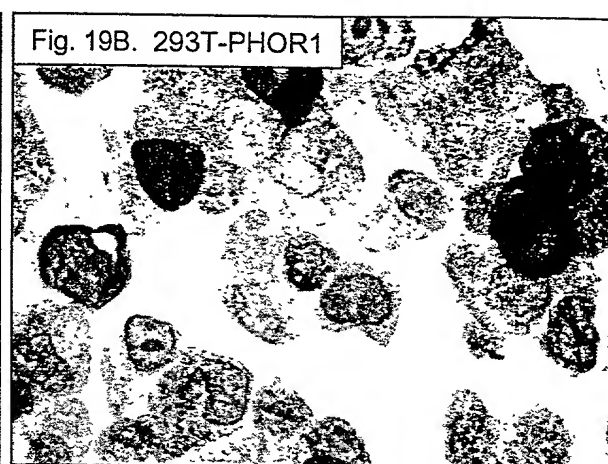


FIG. 20A

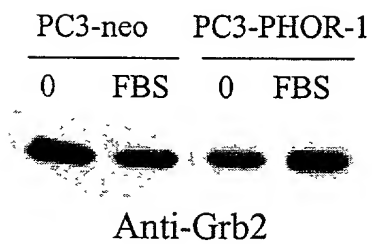
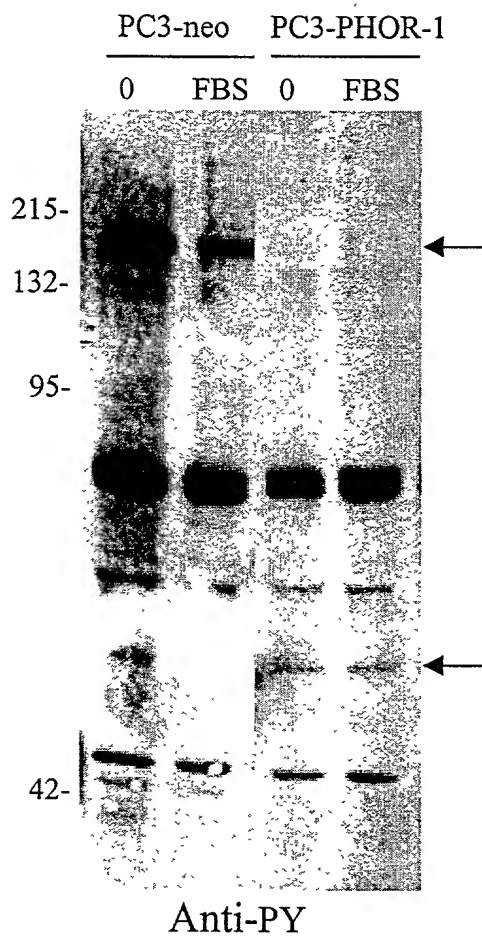


FIG. 20C

FIG. 20B

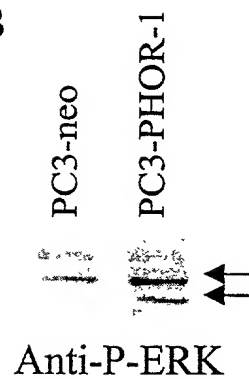


FIG. 20D

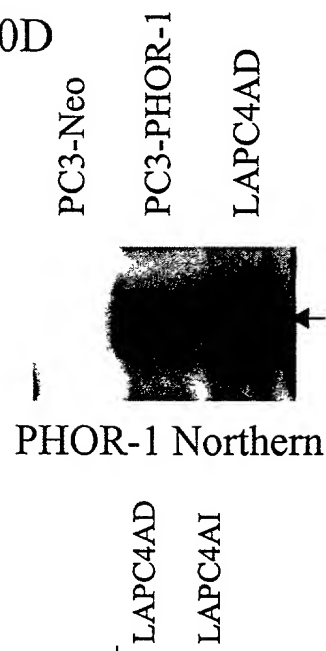


FIG. 20E

PHOR1 Northern

Neo



Fig. 21A

PHOR1



Fig. 21B

Ras

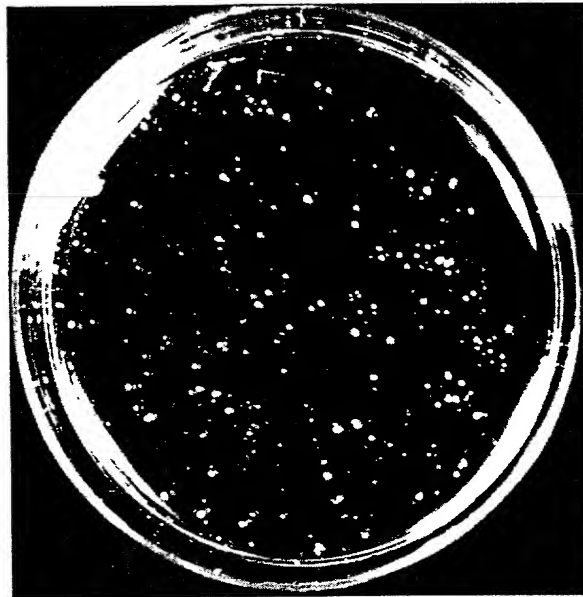


Fig. 21C

FIG. 22

```

5'   9      18      27      36      45      54
GCT GTG GCC ATG TTT ATT GGA GTG TTG GAT CTA TTC TTT ATC ATC CTA TCT TAT
---
A   V   A   M   F   I   G   V   L   D   L   F   F   I   I   L   S   Y

      63      72      81      90      99      108
ATC TTT ATC CTT CAG GCA GTT CTA CAA CTC TCC TCT CAG GAG GCC CGC TAC AAA
---
I   F   I   L   Q   A   V   L   Q   L   S   S   Q   E   A   R   Y   K

      117     126     135     144     153     162
GCA TTT GGG ACA TGT GTC TCT CAC ATA GGT GCC ATC TTA GCC TTC TAC ACA CCT
---
A   F   G   T   C   V   S   H   I   G   A   I   L   A   F   Y   T   P

      171     180     189     198     207     216
TCA GTC ATC TCT TCA GTC ATG CAC CGT GTG GCC CGC TGT GCT GTG CCA CAC GTC
---
S   V   I   S   S   V   M   H   R   V   A   R   C   A   V   P   H   V

      225     234     243     252     261     270
CAC ATT CTC CTC GCC AAT TTC TAT CTG CTC TTC CCA CCC ATG GTC AAT CCC ATC
---
H   I   L   L   A   N   F   Y   L   L   F   P   P   M   V   N   P   I

      279     288     297     306     315     324
ATC TAT GGC GTT AAG ACC AAG CAG ATC CGT GAC AGT CTT GGG AGT ATT CCT GAG
---
I   Y   G   V   K   T   K   Q   I   R   D   S   L   G   S   I   P   E

      333     342     351     360     369     378
AAA GGA TGT GTG AAT AGA GAG TGA GGA ATA AGT GGA AAA AGA GTG GGG CCC AGT
---
K   G   C   V   N   R   E   *

      387     396     405     414     423     432
GAA TGC TGT AGT GGG CCA GGG CTG TGC TGA GAG TAG ATG GGT CCT AGA CTC CAC
---
      441     450     459     468     477     486
GTT TAG TTC TTT TCT TGT ATT ATG AAA AGA ATA AAT GAT GTC CTG AAG CTC AGA
---
      495
AAA AAA AAA AAA AAA 3'
---

```